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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:26:32 ; Search time 151 Seconds

(without alignments)
28.508 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLPVLLAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1 | 54 | 100.0 | 12 | 2 AAY44160 | Membrane- |
| 2 | 54 | 100.0 | 12 | 4 AAE02980 | Hydrophob |
| 3 | 54 | 100.0 | 12 | 4 AAU00644 | Human mem |
| 4 | 54 | 100.0 | 12 | 5 ABG78983 | Cell pene |
| 5 | 54 | 100.0 | 12 | 5 AAU78350 | Grb2 SH2 |
| 6 | 54 | 100.0 | 12 | 5 ABB81929 | Cystic fi |
| 7 | 54 | 100.0 | 12 | 5 ABG75508 | Signal-se |
| 8 | 54 | 100.0 | 12 | 5 ABB81178 | Grb2 SH2 |
| 9 | 54 | 100.0 | 12 | 5 AAU77231 | Synthetic |
| 10 | 54 | 100.0 | 12 | 6 AAE32085 | Transport |
| 11 | 54 | 100.0 | 12 | 7 ADB88787 | Membrane |
| 12 | 54 | 100.0 | 12 | 7 ADC22455 | Protein-d |
| 13 | 54 | 100.0 | 12 | 7 ADG28018 | Kaposi FG |
| 14 | 54 | 100.0 | 12 | 7 ADH76185 | Transduct |
| 15 | 54 | 100.0 | 12 | 7 ADL86654 | MPS (Kapo |
| 16 | 54 | 100.0 | 12 | 7 ADM60178 | Novel rec |
| 17 | 54 | 100.0 | 12 | 8 ADG12916 | Cytoplasm |
| 18 | 54 | 100.0 | 12 | 8 ABG75425 | Kaposi's |
| 19 | 54 | 100.0 | 12 | 8 ABG75438 | Membrane |
| 20 | 54 | 100.0 | 12 | 8 ADJ78876 | Src homol |
| 21 | 54 | 100.0 | 12 | 8 ADL14687 | Cardiant |
| 22 | 54 | 100.0 | 12 | 8 ADK15575 | Membrane |
| 23 | 54 | 100.0 | 12 | 8 ADO26467 | Grb2 SH2 |
| 24 | 54 | 100.0 | 13 | 5 ABG68407 | Membrane |
| 25 | 54 | 100.0 | 14 | 8 ABG75427 | Membrane |

ALIGNMENTS

RESULT 1

AA44160

ID AAY44160 standard; protein; 12 AA.

XX AC AAY44160;

XX AC AAY44160;

DT 01-FEB-2000 (first entry)

DE Membrane-translocating peptide sequence.

XX

Membrane-translocating peptide sequence; MTS; fusion protein; production;
Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;
p53; immune response; hepatitis B virus; surface antigen; canine; feline;
protease inhibitor; cancer; tumor suppressor; bovine.

XX Synthetic.

XX WO9949879-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 99WO-US007189.

XX 31-MAR-1998; 98US-0080083P.

XX 04-NOV-1998; 98US-00186170.

XX (UYVA-) UNIV VANDERBILT.

XX Lin Y, Donahue JP, Rojas M, Tan ZJ;

XX WPI; 1999-610819/52.

XX N-PSDB; AA228749.

XX New peptides containing a membrane-translocating sequence used to develop

products for use in, e.g. vaccines.

XX Claim 1; Page 66; 85pp; English.

This sequence represents a novel membrane-translocating peptide sequence (MTS). The invention relates to the use of the MTS peptides for generating fusion proteins which can be used for the production of polypeptides of interest such as Schistosoma japonicum glutathione S transferase, an adenovirus E3 19K protein or a mammalian p53 protein. Fusions of the peptides can also be used for inducing an immune response in a mammal using e.g. a viral polypeptide such as hepatitis B surface antigen. They can also be used for protecting a subject from an infectious agent using a polypeptide that inhibits reproduction of the infectious agent such as a protease inhibitor. They can also be used for

CC treating cancer using a polypeptide tumor suppressor such as p53 protein
CC or a polypeptide inhibitor of Bcl-2. The methods can be used for treating
CC canine, feline and bovine diseases and also for studying intracellular
CC proteins
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
Db 1 AAVLLPVLAAAP 12

RESULT 2
AAE02980
ID AAE02980 standard; peptide; 12 AA.

XX AAE02980;
XX 10-AUG-2001 (first entry)
XX Hydrophobic protein transduction domain #8.

XX Peptide monomer; nuclear localisation sequence; NLS;
XX Protein transduction domain; PTD; molecule transfer.

XX Unidentified.

XX WO200138547-A2.

XX 31-MAY-2001.

XX 23-NOV-2000; 2000WO-EP011690.

XX 24-NOV-1999; 99EP-00123423.

XX (ROSE/) ROSENECKER J.

XX (RITT/) RITTER W.

XX (RUDO/) RUDOLPH C. M.

XX (PLAN/) PLANK C.

XX Rosenacker J, Ritter W, Rudolph CM, Plank C;

XX WPI; 2001-367696/38.

XX Novel polypeptides comprising at least two monomers which comprise a
XX nuclear localization sequence and protein transduction domain,
XX respectively useful for transferring nucleic acid molecules into
XX eukaryotic cells.

XX Claim 3; Page 32; 68pp; English.

XX The present invention relates to a polypeptide comprising at least two
XX peptide monomers, in which each peptide monomer comprises an amino acid
XX sequence which serves as a nuclear localisation sequence (NLS) or an
XX amino acid sequence which serves as protein transduction domain (PTD) in
XX eukaryotic cells. The polypeptide of the invention is used for
XX transferring a molecule into eukaryotic cells. The use of a polypeptide
XX comprising NLS or PTD drastically increases the efficiency of the
XX transfer of attached molecules, preferably negatively charged molecules
XX into the nucleus or cytoplasm of a eukaryotic cell. The present sequence
XX is hydrophobic PTD which include the sequence of transportan

XX Sequence 12 AA;

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

Db 1 AAVLLPVLAAAP 12

RESULT 3
AAU00644

ID AAU00644 standard; peptide; 12 AA.

XX AAU00644;

XX 07-SEP-2001 (first entry)

XX Human membrane translocating peptide (MTLP) #13.

XX Membrane translocating peptide; MTLP; human; intracellular gene delivery;
XX epithelial cell layer; gastrointestinal tract; circulatory system.

XX Homo sapiens.

XX WO200127154-A2.

XX 19-APR-2001.

XX 27-SEP-2000; 2000WO-IB001491.

XX 27-SEP-1999; 99US-0156246P.

XX (OMAH/) O'MAHONY D J.

XX (LAMB/) LAMBKIN I J.

XX O'mahony DJ, Lambkin IJ;

XX WPI; 2001-300212/31.

XX N-PSDB; AAS00638.

XX Compositions for enhancing uptake of e.g. drugs or DNA across a cell
XX membrane, comprise membrane translocating peptides having specific amino
XX acid sequences or a derivative, fragment, motif, analog or peptidomimetic
XX of the peptides.

XX Claim 2; Page 11; 42pp; English.

XX The sequence represents a human membrane translocated peptide (MTLP).
XX MTLPs and their related fragments, motifs, derivatives and analogues are
XX used for enhancing uptake of a pharmaceutically active agent into a cell,
XX into or out of an intracellular compartment and across a cell layer (for
XX example, an epithelial cell layer lining the gastrointestinal tract),
XX either directly or from a pharmaceutically active agent loaded particle,
XX into the circulatory system of an animal. This method is useful for
XX intracellular gene delivery, as a rapid screening method for the
XX identification of MTLPs which retain the functional activity of a full-
XX length MTLP, as a cell-based screen for assaying the functional activity
XX of a MTLP and characterising the properties of a MTLP, for diagnosis of a
XX pathological disorder (by administration of a MTLP-active agent complex
XX or MTLP-active particle complex comprising a diagnostic agent) and for
XX preventing or treating a pathological disorder

XX Sequence 12 AA;

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

Db 1 AAVLLPVLAAAP 12

RESULT 4

ABG78983

ID ABG78983 standard; peptide; 12 AA.

XX ABG78983;

XX AC ABG78983;

XX 15-NOV-2002 (first entry)
 DT Cell penetrating peptide CPPI.
 DE
 XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma;
 KW sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO200264057-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 15-FEB-2002; 2002WO-US005212.
 PR
 PR 15-FEB-2001; 2001US-0268687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI; 2002-627577/67.
 XX
 PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX
 PS Disclosure; Page 10; 61pp; English.
 XX
 CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is cell penetrating peptide of
 CC the invention
 XX
 SQ Query Match 100.0%; Score 54; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 Db |||||
 1 AAVLLPVLAAAP 12
 RESULT 5
 AAU78350
 ID AAU78350 standard; peptide; 12 AA.

XX AAU78350;
 AC 18-JUN-2002 (first entry)
 DT
 XX Grb2 SH2 domain derived signal peptide.
 DE
 KW Membrane translocation signal; signal sequence based peptide I;
 KW red blood cell vehicle; polypeptide delivery; Grb2; SH2 domain.
 KW
 OS Unidentified.
 XX
 PN WO200207752-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 24-JUL-2001; 2001WO-GB003327.
 XX
 PR 24-JUL-2000; 2000WO-GB002848.
 PR 09-AUG-2000; 2000WO-GB003056.
 PR 01-FEB-2001; 2001WO-GB000417.
 PR 16-FEB-2001; 2001US-00785802.
 XX
 XX (GEND-) GENDEL LTD.
 XX
 PI Craig R;
 XX
 DR WPI; 2002-280593/32.
 XX
 PT Preparing a red blood cell vehicle suitable for delivering an agent to a
 PT target site in a vertebrate due to loading the red blood cell with an
 PT agent-membrane translocation sequence.
 XX
 PS Disclosure; Page 45; 135pp; English.
 XX
 CC The invention describes a method of preparing a red blood cell vehicle
 CC suitable for delivering an agent to a target site in a vertebrate
 CC comprising providing a red blood cell and loading the red blood cell with
 CC an agent-MTS (membrane translocation sequence) conjugate. The red blood
 CC cells produced may be used in the preparation of a medicament for
 CC delivery of an agent to or at a target site and of one or more agents to
 CC a vertebrate. The agent is actively released from the red blood cell
 CC vehicle by application of a stimulus to disrupt the red blood cell
 CC vehicle. This sequence represents signal sequence derived from the Grb2
 CC SH2 domain, one of the membrane translocation peptides tested in the
 CC invention
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 54; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 Db |||||
 1 AAVLLPVLAAAP 12
 RESULT 6
 ABB81929
 ID ABB81929 standard; peptide; 12 AA.
 XX
 AC ABB81929;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Cystic fibrosis fusion protein membrane translocation sequence.
 XX
 KW Cystic fibrosis; transmembrane conductance regulator; CFTR; membrane;
 KW translocation sequence; MTS; gastrointestinal; respiratory; hepatotropic.
 XX
 OS Synthetic.
 XX

XX DR WPI; 2002-280593/32.

XX PT Preparing a red blood cell vehicle suitable for delivering an agent to a

XX PT target site in a vertebrate due to loading the red blood cell with an

XX PT agent-membrane translocation sequence.

XX PS Disclosure; Page 9; 43pp; English.

XX CC The invention discloses a method for preparing a delivery vehicle for

XX CC delivering an agent to a target site in a vertebrate. The method

XX CC comprises loading a cell with an agent-membrane translocation sequence

XX CC (MTS) conjugate, which contains a membrane translocation sequence

XX CC enabling the agent to cross the plasma membrane of a cell. Also disclosed

XX CC is a pharmaceutical composition comprising a red blood cell for delivery

XX CC of an agent to a vertebrate, the red blood cell comprising the novel

XX CC agent-MTS conjugate and a method of immunisation of an animal with an

XX CC antigen. The method is useful for preparing delivery vehicles,

XX CC particularly a red blood cell, for the intracellular delivery of a

XX CC therapeutic agent to a target site. The method is particularly useful for

XX CC enabling an agent to cross the plasma membrane of a target cell, and for

XX CC selectively releasing the agent-MTS conjugate at a target site to

XX CC facilitate the uptake of the agent by the cells at the target site. The

XX CC preferred MTS sequences are from HIV-1 trans-activating protein (Tat),

XX CC Drosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1

XX CC virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a

XX CC Transportan and Amphiphilic model peptide. The sequence presented is the

XX CC Signal-sequence-based peptide III, which is derived from the Grb2 SH2

XX CC (not defined) domain

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0098;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

DB 1 AAVLLPVLAAAP 12

RESULT 8

ABB81178

ID ABB81178 standard; peptide; 12 AA.

AC ABB81178;

DT 25-NOV-2002 (first entry)

DE Grb2 SH2 domain derived peptide fragment.

XX Red blood cell; RBC; virus; vertebrate; therapeutic; tissue imaging;

XX KW Grb2; SH2 domain; membrane translocation.

XX OS Unidentified.

XX WO200260416-A1.

XX PN 08-AUG-2002.

XX PD 01-FEB-2002; 2002WO-GB000437.

XX PF 01-FEB-2001; 2001GB-00002561.

XX PR 16-FEB-2001; 2001US-0269528P.

XX PA (GENE-) GENDEL LTD.

XX PI Mchale AP, Craig R;

XX XX WPI; 2002-643355/69.

XX PT Delivering agent to target site in vertebrate comprises loading red blood

XX PT cell with virus or virus-like particle comprising agent, sensitizing

XX PT

PN WO200258627-A2.

XX PD 01-AUG-2002.

XX PF 09-NOV-2001; 2001WO-US049958.

XX PR 09-NOV-2000; 2000US-0247494P.

XX PA (UYVA-) UNIV VANDERBILT.

XX PI Stecenko A, Brigham K;

XX XX WPI; 2002-590789/63.

XX PT Fusion protein, useful in the treatment of cystic fibrosis or

XX PT dysfunctions of the gastrointestinal tract or liver, comprises cystic

XX PT fibrosis transmembrane conductance regulator and a membrane translocation

XX PT sequence.

XX PS Claim 3; Page 15; 19pp; English.

XX CC The invention relates to a novel fusion protein comprising a cystic

XX CC fibrosis transmembrane conductance regulator (CFTR) and a membrane

XX CC translocation sequence (MTS). The sequence represents the membrane

XX CC translocation sequence. The fusion protein of the invention has

XX CC gastrointestinal, respiratory, and hepatotropic activity. The protein is

XX CC taken up by affected cells and thereby used for treating cystic fibrosis

XX CC or dysfunctions of the gastrointestinal tract or liver

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0098;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

DB 1 AAVLLPVLAAAP 12

RESULT 7

ABG75508

ID ABG75508 standard; peptide; 12 AA.

AC ABG75508;

DT 14-APR-2003 (first entry)

DE Signal-sequence-based peptide III.

XX Translocation; delivery vehicle; agent-membrane translocation sequence;

XX KW MTS; membrane translocation sequence; plasma membrane; red blood cell;

XX KW immunisation; antigen; intracellular delivery; therapeutic; HIV-1;

XX KW trans-activating protein; Tat; Antennapedia homeodomain protein; Antp-HD;

XX KW VP22 protein; HSV-VP22; signal-sequence-based peptide; Transportan;

XX KW Amphiphilic model peptide; Grb2 SH2.

XX OS Unidentified.

XX PN US2002151004-A1.

XX PD 17-OCT-2002.

XX PF 16-FEB-2001; 2001US-00785802.

XX PR 24-JUL-2000; 2000WO-GB002848.

XX PR 09-AUG-2000; 2000WO-GB003056.

XX PR 22-DEC-2000; 2000US-00748063.

XX PR 22-DEC-2000; 2000US-00748789.

XX PA (CRAI/) CRAIG R.

XX PI Craig R;

PT cell, introducing cell into vertebrate and applying energy to release
PT virus particle from cell.
PS Disclosure; Page 55; 87pp; English.
XX
CC The invention relates to delivering an agent to a target site in a
CC vertebrate. The method involves (a) loading a red blood cell (RBC) with a
CC virus or a virus-like particle (VLP) comprising an agent; (b) sensitizing
CC RBC to render it more susceptible to disruption than unsensitized RBC;
CC (c) introducing RBC into a vertebrate, and (d) applying energy to release
CC (i). Steps (a) and (b) may be performed in any order. (ii) (RBC loaded
CC with a virus or a virus-like particle comprising a therapeutic agent) is
CC useful for the delivery of a therapeutic agent to a target site in a
CC vertebrate, or in the preparation of a medicament for delivery of a
CC therapeutic agent to a target site in a vertebrate. (ii) is also useful
CC for delivering one or more agents to a vertebrate and for treating or
CC preventing a disease. The method is useful for delivering agents such as
CC those useful for imaging of tissues in vivo or ex vivo, preferably for
CC delivering an agent to a subcellular organelle such as nucleus,
CC mitochondria, Golgi or endoplasmic reticulum. The present sequence
CC represents a Grb2 SH2 domain derived peptide fragment, used for membrane
CC translocation
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLAAAP 12
DB 1 AAVLLPVLAAAP 12
|||||
RESULT 9
AAU77231
ID AAU77231 standard; peptide; 12 AA.
XX
AC AAU77231;
XX
DT 05-JUN-2002 (first entry)
XX
DE Synthetic pCDNA3-E7/MTS peptide sequence.
XX
KW Virucide; cytostatic; vaccine; intercellular transport; antigenic;
KW immune response; cytotoxic T lymphocyte; tumour; cancer; pCDNA3-E7/MTS;
KW chronic viral infection; veterinary herpesvirus infection; pseudorabies;
KW equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
KW fowl; animal retroviral disease; rabies.
XX
OS Synthetic.
XX
XX WO200209645-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US023966.
XX
XX 01-AUG-2000; 2000US-0222185P.
XX
XX 15-FEB-2001; 2001US-0268575P.
XX
XX 04-APR-2001; 2001US-0281004P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Wu T, Hung C;
XX
XX WPI; 2002-257367/30.
XX
XX N-PSDB; ABK11804.
XX
XX New nucleic acids encoding fusion polypeptide comprising intercellular
XX transport polypeptide linked to antigenic polypeptide, useful as
XX therapeutic vaccine for cancer and major chronic viral infections.
XX

PS Example 1; Page 39; 102pp; English.
XX
CC The present invention relates to a new nucleic acid molecule that encodes
CC a fusion polypeptide. The fusion protein comprises a first polypeptide
CC comprising at least one intercellular transport polypeptide and a second
CC polypeptide comprising at least one antigenic polypeptide or peptide. The
CC invention also describes an optional linker peptide linking the first and
CC second polypeptide. The nucleic acid is useful as a vaccine for enhancing
CC immune responses, primarily cytotoxic T lymphocyte responses to specific
CC antigens such as tumour or viral antigens. The compositions comprising
CC the nucleic acids are especially useful as a therapeutic vaccine for
CC cancer and for major chronic viral infections, as well as in the
CC treatment of veterinary herpesvirus infections, including equine or
CC bovine herpesvirus, Marek's disease virus in chickens and other fowls,
CC animal retroviral diseases, pseudorabies and rabies. The present amino
CC acid sequence represents the peptide used in the methods of the invention
CC for the generation of pCDNA3-E7/MTS expression vector
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLAAAP 12
DB 1 AAVLLPVLAAAP 12
|||||
RESULT 10
AAE32065
ID AAE32065 standard; peptide; 12 AA.
XX
AC AAE32065;
XX
DT 24-MAR-2003 (first entry)
XX
DE Transport peptide used in the invention.
XX
KW Drug delivery construct; axon growth; nerve injury; ischaemic damage;
KW stroke injury; gene therapy; neuroleptic; neuroprotective.
XX
OS Unidentified.
XX
XX WO200283179-A2.
XX
XX 24-OCT-2002.
XX
XX 08-APR-2002; 2002WO-CA000480.
XX
XX 12-APR-2001; 2001CA-02342970.
XX
XX 13-NOV-2001; 2001CA-02362004.
XX
XX 15-JAN-2002; 2002CA-02367636.
XX
XX (BIOA-) BIOAXONE THERAPEUTIQUE INC.
XX
XX McKerracher L;
XX
XX WPI; 2003-092963/08.
XX
XX New drug delivery construct comprising a transport and active agent for
XX treating nerve injury.
XX
XX Disclosure; Page 52; 189pp; English.
XX
XX The invention relates to a new drug delivery construct comprising at least
XX one transport agent region and an active agent region. The transport
XX agent region is able to facilitate the uptake of the active agent region
XX into a cell. The active agent region is an active therapeutic agent
XX region able to facilitate axon growth and an analogue. The drug delivery
XX construct is useful for suppressing the inhibition of neuronal axon
XX growth, facilitating axon growth, treating nerve injury, treating

CC ischaemic damage related to stroke injury. The drug delivery construct
CC and the drug conjugate are useful for the manufacture of a pharmaceutical
CC composition for treating nerve injury. The invention is useful in gene
CC therapy. The present sequence is transport peptide used in the invention
XX
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12
RESULT 11
ID ADB88787 standard; peptide; 12 AA.
XX
AC ADB88787;
XX
DT 04-DEC-2003 (first entry)
XX
DE Membrane translocating peptide #13.
XX
KW Peyer's patch cell; non-Peyer's patch cell; transcription factor;
KW upregulated protein; antigen; vaccine delivery; M cell;
KW membrane translocating peptide.
XX
OS Unidentified.
XX
PN WO2003004646-A2.
XX
PD 16-JAN-2003.
XX
PF 04-APR-2002; 2002WO-IB003866.
XX
PR 04-APR-2001; 2001US-0281387P.
XX
PR 02-JUL-2001; 2001US-0302591P.
XX
XX (OMAH/) O'MAHONY D J.
XX
PI O'mahony DJ, Byrne D, Brayden D;
XX
XX WPI; 2003-229409/22.
XX
PT Increasing the levels of a protein in a Peyer's patch cell, useful for
PT targeted vaccine or drug delivery, comprises delivering to the Peyer's
PT patch cell a transcription factor or an activator of a transcription
PT factor.
XX
PS Example 6; Page 51; 147pp; English.
XX
CC The invention relates to a novel method for increasing the levels of a
CC protein in a Peyer's patch cell. The method comprises delivering to the
CC cell a nucleic acid coding for a protein, the level of which or its mRNA
CC is greater than in a non-Peyer's patch cell. The preferred protein of the
CC invention is a transcription factor or a protein that activates a
CC transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3
CC -signal transducer and activator of transcription 3, NFkappaBgr; Tf p105
CC subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside
CC diphosphate kinase B, metataseis reducing protein, and C-est-J proto-
CC oncogene, and p54. The preferred upregulated protein of the invention is
CC selected from clusterin, T-cell surface glycoprotein CD5 precursor, Hsp
CC 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a
CC protein selected from the group. The method is useful for increasing or
CC decreasing the level of a protein in a Peyer's patch cell, particularly
CC in increasing antigen or vaccine delivery to M cells. The method may also
CC be used to enhance transport of a drug through the gastrointestinal tract
CC (GIT). This sequence represents a membrane translocating peptide of the
CC invention.
XX

SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12
RESULT 12
ID ADC22455 standard; peptide; 12 AA.
XX
AC ADC22455;
XX
DT 18-DEC-2003 (first entry)
XX
DE Protein-derived transport peptide SEQ ID NO:304.
XX
KW recombinant fusion protein; fusion protein; binding; detection;
KW localisation domain; binding domain;
KW subcellular compartment localisation.
XX
OS Synthetic.
XX
PN WO2003012068-A2.
XX
PD 13-FEB-2003.
XX
PF 01-AUG-2002; 2002WO-US024572.
XX
PR 01-AUG-2001; 2001US-0309395P.
XX
PR 13-DEC-2001; 2001US-0341589P.
XX
XX (CELL-) CELLOMICS INC.
XX
XX Bright G, Premkumar DR, Chen Y;
XX WPI; 2003-248174/24.
XX
PT New recombinant fusion protein comprising detection and first
PT localization domains and a binding domain for the molecule of interest,
PT useful for detecting binding of a molecule of interest.
XX
PS Disclosure; SEQ ID NO 304; 101pp; English.
XX
CC The present invention describes a recombinant fusion protein (I) for
CC detecting binding of a molecule of interest. (I) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC molecule of interest is separated from the first localisation domain by 0
CC -20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is
CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
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 DB 1 AAVLLPVLLAAP 12

RESULT 13
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 ID ADG28018 standard; peptide; 12 AA.
 XX
 AC ADG28018;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Kaposi FGF signal membrane fusion sequence seq id 19.
 XX
 KW fusion protein; cold shock domain; membrane translocation sequence; CspA;
 KW CspB; CspC; CspD; rpi S1 binding domain; eukaryotic Y-box protein;
 KW DNA binding protein B; DBPB; DBPA; EFE-1; mRNP3; mRNP4; FRG Y1;
 KW nuclease-sensitive element binding protein 1; NSEP 1;
 KW DNA condensation domain; DNA binding domain; SPKR;
 KW nuclear localisation sequence; NLS; protein purification tagged sequence;
 KW gene delivery; kaposi's sarcoma-associated herpesvirus;
 KW FGF signal sequence; membrane fusion sequence.
 XX
 OS Human herpesvirus 8.
 XX
 XX
 PN US2003211590-A1.
 XX
 PD 13-NOV-2003.
 XX
 PF 13-MAY-2002; 2002US-00144549.
 XX
 PR 13-MAY-2002; 2002US-00144549.
 XX
 PA (HWUP/) HWU P L.
 XX
 PI Hwu PL;
 DR WPI; 2003-901590/82.
 XX
 PT New fusion protein comprising a cold shock domain, and a membrane
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
 PT cells for gene delivery.
 XX
 PS Claim 9; SEQ ID NO 19; 24pp; English.
 XX
 CC The invention describes a fusion protein for delivery of a desired
 CC molecule into cells or nuclei, comprising a cold shock domain, its
 CC homologue and functional derivative, and a membrane translocation
 CC sequence or its functional equivalent peptides and/or derivatives. The
 CC fusion protein comprises a cold shock domain that is selected from CspA,
 CC CspB, CspC, CspD, rpi S1 binding domain, eukaryotic Y-box proteins, DNA
 CC binding protein B (DBPB), DBPA, EFE-1, mRNP3, mRNP4, FRG Y1 and nuclease-
 CC sensitive element binding protein 1 (NSEP 1). The functional equivalent
 CC derivative of cold shock protein is modified by inserting into the cold
 CC shock domain with a DNA condensation domain or a DNA binding domain. The
 CC DNA condensation or binding domain is selected from DNA condensation
 CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences
 CC (NLS+). The membrane transduction sequence is protein transduction domain
 CC (PTD) or membrane fusion sequence. The fusion protein further comprises a
 CC protein purification tagged sequence selected from HA, GST, and His6 tag.
 CC The fusion protein is useful for delivering DNAs and RNAs to in vivo
 CC cells for gene delivery or for delivering nucleic acids to an embryo or
 CC to a living animal for the production of transgenic animal. This is the
 CC amino acid sequence of a membrane fusion sequence derived from Kaposi's
 CC sarcoma-associated herpesvirus FGF signal sequence.

SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
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 DB 1 AAVLLPVLLAAP 12

RESULT 14
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 AC ADH76185;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Transduction domain peptide of the invention SEQ ID NO:286.
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 KW heat shock protein 20; cytosolic; antiarteriosclerotic; vasotropic;
 KW antianginal; cerebroprotective; antiarrhythmic; antiasthmatic;
 KW gynaecological; hypotensive; antimigraine; relaxant; HSP;
 KW smooth muscle cell; smooth muscle cell; transduction domain.
 XX
 OS Synthetic.
 XX
 PN WO2003018758-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-US026918.
 XX
 PR 23-AUG-2001; 2001US-0314535P.
 XX
 PA (UYAR-) UNIV ARIZONA.
 PA (BROP/) BROPHY C.
 PA (KOMA/) KOMALAVILAS P.
 PA (PANI/) PANITCH A.
 PA (SEAL/) SEAL B.
 PA (LOKE/) LOKESH J.
 XX
 PI Brophy C, Komalavilas P, Panitch A, Seal B, Lokesh J;
 DR WPI; 2003-393248/37.
 XX
 PT New heat shock protein 20-derived polypeptides, useful for inhibiting,
 PT treating or preventing smooth muscle cell vasospasm or a disorder such as
 PT intimal hyperplasia, restenosis, atherosclerosis or smooth muscle cell
 PT tumors.
 XX
 PS Claim 29; SEQ ID NO 286; 194pp; English.
 XX
 CC The invention relates to a novel polypeptide comprising a heat shock
 CC protein 20-derived polypeptide. A polypeptide of the invention has
 CC cytosolic, antiarteriosclerotic, vasotropic, antianginal,
 CC cerebroprotective, antiarrhythmic, antiasthmatic, gynaecological,
 CC hypotensive, antimigraine, tocolytic, and relaxant activity, and may act
 CC as a HSP agonist or antagonist. The polypeptides, heat shock protein
 CC (HSP) 20, and methods are useful for treating or preventing a disorder,
 CC e.g. intimal hyperplasia, stenosis, restenosis, transplant vasculopathy,
 CC atherosclerosis, smooth muscle cell tumours such as leiomyosarcoma, or
 CC vasospasm, which is associated with angina, coronary vasospasm,
 CC Prinzmetal's angina, coronary ischaemia, stroke, bradycardia,
 CC hypertension, pulmonary (lung) hypertension, asthma (bronchospasm),
 CC toxemia of pregnancy, pre-term labour, pre-eclampsia/eclampsia, Raynaud's
 CC disease, Raynaud's phenomenon, haemolytic-uremia, non-occlusive
 CC mesenteric ischaemia, anal fissure, achalasia, impotence, migraine, or
 CC ischaemic muscle injury associated with smooth muscle spasm. The
 CC polypeptides and HSP 20 are also useful for inhibiting smooth muscle cell
 CC proliferation and/or migration. The present sequence represents a peptide
 CC used in a polypeptide of the invention.

Fri Feb 4 11:21:31 2005

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XX Sequence 12 AA;
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Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 15
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ID ADL8654 standard; peptide; 12 AA.
XX
AC ADL8654;
XX
DT 20-MAY-2004 (first entry)
XX
DE MPS (Kaposi FGF signal sequence) membrane fusion sequence peptide 2.
XX
KW fusion protein; cold shock domain; membrane translocation; gene therapy;
XX transgenic; membrane fusion; MPS; Kaposi FGF signal.
XX
OS Unidentified.
XX
PN JP2004035409-A.
XX
PD 05-FEB-2004.
XX
PF 15-MAY-2002; 2002JP-00140441.
XX
PR 13-MAY-2002; 2002US-00144549.
XX
PA (GENE-) GENESHUTTLE BIOPHARM INC.
XX
PI Hwu PL;
XX
DR WPI; 2003-901590/82.
XX
PT New fusion protein comprising a cold shock domain, and a membrane
PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
PT cells for gene delivery.
XX
PS Claim 9; SEQ ID NO 17; 53pp; Japanese.
XX
CC The invention relates to a novel fusion protein for delivery of a desired
CC molecule into cells or nuclei comprising a cold shock domain, its
CC homologue and functional derivative and a membrane translocation sequence
CC or its functionally equivalent peptides and/or derivatives. The fusion
CC protein of the invention may be useful for delivering DNAs and RNAs to in
CC vivo cells for gene therapy or for delivering nucleic acids to an embryo
CC or to a living animal for the production of transgenic animals. The
CC current sequence is that of a membrane fusion sequence peptide of the
CC invention.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

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Search completed: February 2, 2005, 18:40:47
Job time : 153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:44:19 ; Search time 144 Seconds
(without alignments)
30.107 Million cell updates/sec

Title: US-10-634-645-1
Perfect score: 54
Sequence: 1 AAVLLPVLLAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 54 | 100.0 | 12 | 9 | US-09-789-836-12 |
| 2 | 54 | 100.0 | 12 | 9 | US-09-785-802A-10 |
| 3 | 54 | 100.0 | 12 | 10 | US-09-997-455B-4 |
| 4 | 54 | 100.0 | 12 | 13 | US-10-116-288-1 |
| 5 | 54 | 100.0 | 12 | 14 | US-10-226-956-286 |
| 6 | 54 | 100.0 | 12 | 14 | US-10-077-555-1 |
| 7 | 54 | 100.0 | 12 | 14 | US-10-211-088-304 |
| 8 | 54 | 100.0 | 12 | 14 | US-10-156-570A-27 |
| 9 | 54 | 100.0 | 12 | 14 | US-10-126-845-1 |
| 10 | 54 | 100.0 | 12 | 14 | US-10-126-845-14 |
| 11 | 54 | 100.0 | 12 | 14 | US-10-126-845-72 |
| 12 | 54 | 100.0 | 12 | 14 | US-10-136-187-1 |
| 13 | 54 | 100.0 | 12 | 14 | US-10-116-275-102 |

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| 14 | 54 | 100.0 | 12 | 14 | US-10-144-549-19 |
| 15 | 54 | 100.0 | 12 | 15 | US-10-361-208-473 |
| 16 | 54 | 100.0 | 12 | 15 | US-10-212-410-2 |
| 17 | 54 | 100.0 | 12 | 15 | US-10-416-285-1 |
| 18 | 54 | 100.0 | 12 | 16 | US-10-764-235-1 |
| 19 | 54 | 100.0 | 12 | 16 | US-10-764-235-14 |
| 20 | 54 | 100.0 | 12 | 16 | US-10-751-380-8 |
| 21 | 54 | 100.0 | 13 | 14 | US-10-013-815-20 |
| 22 | 54 | 100.0 | 15 | 14 | US-10-126-845-2 |
| 23 | 54 | 100.0 | 15 | 14 | US-10-126-845-3 |
| 24 | 54 | 100.0 | 15 | 14 | US-10-126-845-60 |
| 25 | 54 | 100.0 | 15 | 14 | US-10-126-845-61 |
| 26 | 54 | 100.0 | 15 | 14 | US-10-136-187-2 |
| 27 | 54 | 100.0 | 15 | 14 | US-10-136-187-4 |
| 28 | 54 | 100.0 | 15 | 14 | US-10-136-187-6 |
| 29 | 54 | 100.0 | 15 | 14 | US-10-136-187-8 |
| 30 | 54 | 100.0 | 15 | 14 | US-10-136-187-12 |
| 31 | 54 | 100.0 | 15 | 14 | US-10-136-187-13 |
| 32 | 54 | 100.0 | 15 | 14 | US-10-136-187-29 |
| 33 | 54 | 100.0 | 15 | 14 | US-10-136-187-33 |
| 34 | 54 | 100.0 | 15 | 14 | US-10-136-187-34 |
| 35 | 54 | 100.0 | 15 | 14 | US-10-136-187-35 |
| 36 | 54 | 100.0 | 15 | 14 | US-10-136-187-36 |
| 37 | 54 | 100.0 | 15 | 14 | US-10-136-187-37 |
| 38 | 54 | 100.0 | 15 | 14 | US-10-136-187-38 |
| 39 | 54 | 100.0 | 15 | 14 | US-10-136-187-39 |
| 40 | 54 | 100.0 | 15 | 16 | US-10-764-235-2 |
| 41 | 54 | 100.0 | 16 | 14 | US-10-126-845-5 |
| 42 | 54 | 100.0 | 16 | 14 | US-10-126-845-48 |
| 43 | 54 | 100.0 | 16 | 14 | US-10-126-845-63 |
| 44 | 54 | 100.0 | 16 | 14 | US-10-136-187-3 |
| 45 | 54 | 100.0 | 16 | 14 | US-10-136-187-7 |

ALIGNMENTS

RESULT 1
US-09-789-836-12
; Sequence 12, Application US/09789836
; Patent No. US20020082204A1
; GENERAL INFORMATION:
; APPLICANT: BRIGHAM, KENNETH L.
; APPLICANT: STECENKO, ARLENE A.
; APPLICANT: SEALY, LINDA
; TITLE OF INVENTION: TREATMENT OF INFLAMMATION WITH P20
; FILE REFERENCE: N-6977
; CURRENT APPLICATION NUMBER: US/09/789,836
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/183,584
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-789-836-12

Query Match 100.0%; Score 54; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 2
US-09-785-802A-10
; Sequence 10, Application US/09785802A

Fri Feb 4 11:21:31 2005

us-10-634-645-1.rapb

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; Patent No. US20020151004A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; FILE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/748,789
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
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US-09-785-802A-10

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Best Local Similarity 100.0%; Pred. No. 0.03;
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Db 1 AAVLLPVLLAAP 12

RESULT 3
US-09-997-465B-4
; Sequence 4, Application US/09997465B
; Publication No. US20030118610A1
; GENERAL INFORMATION:
; APPLICANT: Stern, William
; APPLICANT: Mehta, No. US20030118610A1er M.
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRAN
; TITLE OF INVENTION: TRANSLOCATORS
; FILE REFERENCE: P/546-247
; CURRENT APPLICATION NUMBER: US/09/997,465B
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 22
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; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-465B-4

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Db 1 AAVLLPVLLAAP 12

RESULT 4
US-10-116-288-1
; Sequence 1, Application US/10116288
; Publication No. US20020143142A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.0097U3
; CURRENT APPLICATION NUMBER: US/10/116,288
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/562,868

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; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288-1

Query Match 100.0%; Score 54; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
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Db 1 AAVLLPVLLAAP 12

RESULT 5
US-10-226-956-286
; Sequence 286, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-286

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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVLLPVLLAAP 12

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RESULT 6
US-10-077-555-1
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; Publication No. US20030077289A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Use of Cell-Penetrating Peptides to Generate Antitumor Immunity
; FILE REFERENCE: P02373US1/10200806
; CURRENT APPLICATION NUMBER: US/10/077,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/268,687
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-077-555-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAVLLPVLAAAP 12

RESULT 7
US-10-211-088-304
; Sequence 304, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-304

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | | | |
DB 1 AAVLLPVLAAAP 12

RESULT 8
US-10-156-570A-27
; Sequence 27, Application US/10156570A
; Publication No. US20030125242A1
; GENERAL INFORMATION:
; APPLICANT: ROSENECKER, JOSEPH
; APPLICANT: RITTER, WOLFGANG

; APPLICANT: RUDOLPH, CARSTEN MARTIN
; APPLICANT: PLANK, CHRISTIAN
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR
; TITLE OF INVENTION: LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS
; TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: INTO CELLS
; FILE REFERENCE: VOS-35
; CURRENT APPLICATION NUMBER: US/10/156,570A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: PCT/EP00/11690
; PRIOR FILING DATE: 2000-11-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: transportan
; OTHER INFORMATION: hydrophobic protein transduction domain
US-10-156-570A-27

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
| | | | | | | | | | | |
DB 1 AAVLLPVLAAAP 12

RESULT 9
US-10-126-845-1
; Sequence 1, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-10-126-845-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
| | | | | | | | | | | |
DB 1 AAVLLPVLAAAP 12

RESULT 10
US-10-126-845-14
; Sequence 14, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

Fri Feb 4 11:21:31 2005

us-10-634-645-1.rapb

```

; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-10-126-845-14

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 11
US-10-126-845-72
; Sequence 72, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 72
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(12)
; OTHER INFORMATION: D form amino acid
US-10-126-845-72

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 12
US-10-136-187-1
; Sequence 1, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/287,786

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; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-136-187-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 13
US-10-116-275-102
; Sequence 102, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 102
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-102

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 14
US-10-144-549-19
; Sequence 19, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
; APPLICANT: Geneshuttle Biopharm, Inc.
; APPLICANT: Hwu, Paul L.
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
; FILE REFERENCE: MBHB 02-340
; CURRENT APPLICATION NUMBER: US/10/144,549
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus

```

; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Kaposi FGF signal sequence.
US-10-144-549-19

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 15

US-10-361-208-473
; Sequence 473, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
; FILE REFERENCE: 0050.2041-003
; CURRENT APPLICATION NUMBER: US/10/361,208
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 473
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-361-208-473

Query Match 100.0%; Score 54; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

Search completed: February 2, 2005, 18:56:44
Job time : 144 secs

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| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|------------------|--------------------|
| | Score | Match | Length | | | |
| 1 | 54 | 100.0 | 12 | 3 | US-09-186-170-1 | Sequence 1, Appli |
| 2 | 54 | 100.0 | 12 | 4 | US-09-562-868-1 | Sequence 1, Appli |
| 3 | 54 | 100.0 | 12 | 4 | US-09-997-4638-4 | Sequence 4, Appli |
| 4 | 54 | 100.0 | 12 | 4 | US-10-083-889-8 | Sequence 8, Appli |
| 5 | 54 | 100.0 | 12 | 4 | US-10-116-288-1 | Sequence 1, Appli |
| 6 | 54 | 100.0 | 12 | 4 | US-09-671-089-1 | Sequence 1, Appli |
| 7 | 54 | 100.0 | 12 | 4 | US-09-671-089-14 | Sequence 14, Appli |
| 8 | 54 | 100.0 | 15 | 4 | US-09-671-089-2 | Sequence 2, Appli |
| 9 | 54 | 100.0 | 16 | 4 | US-09-671-089-3 | Sequence 3, Appli |
| 10 | 54 | 100.0 | 16 | 4 | US-09-671-089-5 | Sequence 5, Appli |
| 11 | 54 | 100.0 | 16 | 4 | US-09-671-089-48 | Sequence 48, Appli |
| 12 | 54 | 100.0 | 19 | 4 | US-09-671-089-4 | Sequence 4, Appli |
| 13 | 50 | 92.6 | 11 | 3 | US-09-186-170-9 | Sequence 9, Appli |
| 14 | 50 | 92.6 | 11 | 4 | US-09-562-868-9 | Sequence 9, Appli |
| 15 | 50 | 92.6 | 11 | 4 | US-10-116-288-9 | Sequence 9, Appli |
| 16 | 50 | 92.6 | 11 | 4 | US-09-671-089-19 | Sequence 19, Appli |
| 17 | 50 | 92.6 | 13 | 4 | US-09-671-089-10 | Sequence 10, Appli |
| 18 | 47 | 87.0 | 11 | 3 | US-09-186-170-5 | Sequence 5, Appli |
| 19 | 47 | 87.0 | 11 | 4 | US-09-562-868-5 | Sequence 5, Appli |
| 20 | 47 | 87.0 | 11 | 4 | US-10-116-288-5 | Sequence 5, Appli |
| 21 | 47 | 87.0 | 11 | 4 | US-09-671-089-15 | Sequence 15, Appli |
| 22 | 47 | 87.0 | 13 | 4 | US-09-671-089-6 | Sequence 6, Appli |
| 23 | 47 | 87.0 | 17 | 4 | US-09-671-089-23 | Sequence 23, Appli |
| 24 | 46 | 85.2 | 10 | 3 | US-09-186-170-8 | Sequence 8, Appli |
| 25 | 46 | 85.2 | 10 | 4 | US-09-562-868-8 | Sequence 8, Appli |
| 26 | 46 | 85.2 | 10 | 4 | US-10-116-288-8 | Sequence 8, Appli |
| 27 | 46 | 85.2 | 10 | 4 | US-09-671-089-20 | Sequence 20, Appli |

Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 4
US-10-083-889-8
; Sequence 8, Application US/10083889
; Patent No. 6673894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mammalian
US-10-083-889-8

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 5
US-10-116-288-1
; Sequence 1, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6780843
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/562,968
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.

US-09-562-868-1
; Sequence 1, Application US/09562868
; Patent No. 6432680
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6432680
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009702
; CURRENT APPLICATION NUMBER: US/09/562,868
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-09-562-868-1

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 3
US-09-997-465B-4
; Sequence 4, Application US/09997465B
; Patent No. 6673574
; GENERAL INFORMATION:
; APPLICANT: Stern, William
; APPLICANT: Mehta, No. 6673574er M.
; APPLICANT: Ray, Martha V.L.
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRAN
; TITLE OF INVENTION: TRANSLOCATORS
; FILE REFERENCE: P/546-247
; CURRENT APPLICATION NUMBER: US/09/997,465B
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-997-465B-4

Query Match 100.0%; Score 54; DB 4; Length 12;

; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288-1

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12

RESULT 6

US-09-671-089-1
; Sequence 1, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-1

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12

RESULT 7

US-09-671-089-14
; Sequence 14, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-14

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12

RESULT 8

US-09-671-089-2
; Sequence 2, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
; NAME/KEY: MOD RES
; LOCATION: (15)..
; OTHER INFORMATION: linked to FITC-LC
US-09-671-089-2

Query Match 100.0%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
DB 4 AAVLLPVLLAAP 15

RESULT 9

US-09-671-089-3
; Sequence 3, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-3

Query Match 100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

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Fri Feb 4 11:21:31 2005

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Db      5 AAVLLPVLLAAP 16
|||||
RESULT 10
US-09-671-089-5
; Sequence 5, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic
US-09-671-089-5
Query Match      100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAVLLPVLLAAP 12
|||||
Db      4 AAVLLPVLLAAP 15
|||||
RESULT 11
US-09-671-089-48
; Sequence 48, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dansylated membrane translocating peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: dansylated
US-09-671-089-48
Query Match      100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAVLLPVLLAAP 12
|||||
Db      5 AAVLLPVLLAAP 16
|||||
RESULT 12
US-09-671-089-4
; Sequence 4, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-4
Query Match      100.0%; Score 54; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAVLLPVLLAAP 12
|||||
Db      4 AAVLLPVLLAAP 15
|||||
RESULT 13
US-09-186-170-9
; Sequence 9, Application US/09186170
; Patent No. 6248558
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6248558
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: VU9841
; CURRENT APPLICATION NUMBER: US/09/186,170
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/080,083
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; PUBLICATION INFORMATION:
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
; RELEVANT RESIDUES: 1 TO 12
US-09-186-170-9
Query Match      92.6%; Score 50; DB 3; Length 11;

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Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
Db 1 AVLLPVLLAAP 11

RESULT 14

US-09-562-868-9
; Sequence 9, Application US/09562868
; Patent No. 6432680
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6432680
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009702
; CURRENT APPLICATION NUMBER: US/09/562,868
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(11)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
; SOFTWARE: Patentin Ver. 2.0
US-09-562-868-9

Query Match 92.6%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
Db 1 AVLLPVLLAAP 11

RESULT 15

US-10-116-288-9
; Sequence 9, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6780843
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288

; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/562,868
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(11)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
; SOFTWARE: Patentin Ver. 2.0
US-10-116-288-9

Query Match 92.6%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
Db 1 AVLLPVLLAAP 11

Search completed: February 2, 2005, 18:45:41
Job time : 39 secs

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RESULT 4

AB3032
hypothetical protein Atu3863 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB3032
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3032
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <KUR>
A:Cross-references: UNIPROT:Q8U966; GB:AE008689; PIDN:AAL44672.1; PID:g17742298; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3863
A:Map position: linear chromosome

| | | | | |
|-----------------------|-------|---------------|-------|-------------|
| Query Match | 72.2% | Score 39; | DB 2; | Length 493; |
| Best Local Similarity | 63.6% | Pred. No. 38; | | |
| Matches | 7; | Conservative | 3; | Mismatches |
| | | | 1; | Indels |
| | | | 0; | Gaps |
| | | | 0; | |

QY 2 AVLLPVLLAAP 12
||: ||: |||
Db 190 AVVAPILIAAP 200

RESULT 5

A96254
exsE protein (AJ225561) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A96254
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman
; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the plant Pathogen and Biotechnology Agent Agrobacterium tu
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A96254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-602 <KUR>
A:Cross-references: UNIPROT:Q8U966; GB:AE007870; PIDN:AAK89555.1; PID:g15159439; GSPDB:
C:Genetics:
A:Gene: AGR_L 1966
A:Map position: linear chromosome

| | | | | |
|-----------------------|-------|---------------|-------|-------------|
| Query Match | 72.2% | Score 39; | DB 2; | Length 602; |
| Best Local Similarity | 63.6% | Pred. No. 46; | | |
| Matches | 7; | Conservative | 3; | Mismatches |
| | | | 1; | Indels |
| | | | 0; | Gaps |
| | | | 0; | |

QY 2 AVLLPVLLAAP 12
||: ||: |||
Db 299 AVVAPILIAAP 309

RESULT 6

B44102
di-N-acetylchitinase (EC 3.2.1.1) - bovine (fragment)
N:Alternate names: chitinase; lysosomal glycosidase
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Mar-1997
C:Accession: B44102
R:Fisher, K.J.; Aronson Jr., N.N.
T:Biochem. 267, 19607-19616, 1992

A:Title: Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase
 A:Reference number: A44102; MUID:92406917; PMID:1527079
 A:Accession: B44102

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <FIS>

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIP:113986)

C:Keywords: glycosidase; hydrolase

Query Match 70.4%; Score 38; DB 2; Length 175;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

DB 23 APLLLPVLAAAP 34

RESULT 7

T35589 probable secreted protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T35589; S37564

R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z1583

A:Accession: T35589

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-249 <SAU>

A:Cross-references: UNIPROT:P40179; EMBL:AL031317; PIDN:CAA20416.1; GSPDB:GN00070; SCOE

A:Experimental source: strain A3(2)

R:Duclene, A.M.; Kieser, K.; Hopwood, D.; Thompson, C.; Mazodier, P.

submitted to the EMBL Data Library, September 1993

A:Description: Molecular characterization of two groEL genes in Streptomyces coelicolor

A:Reference number: S37564

A:Accession: S37564

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 121-249 <DUC>

A:Cross-references: EMBL:X75206; NID:g406595; PIDN:CAA53017.1; PID:g406596

C:Genetics:

A:Gene: SCOE:SC6G4.38

Query Match 70.4%; Score 38; DB 2; Length 249;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

DB 14 AALLPVLAAAP 25

RESULT 8

AF3275

A:Species: Brucella melitensis

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AF3275

R:DelVecchio, V.G.; Kapral, R.J.; Patra, G.; Muir, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AF3275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <KUR>

A:Cross-references: UNIPROT:Q8YJ99; GB:AE008917; PIDN:AAL51369.1; PID:g17982069; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0187
 A:Map position: 1

Query Match 70.4%; Score 38; DB 2; Length 297;
 Best Local Similarity 80.0%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 10

DB 161 AALLPVLAA 170

RESULT 9

C82614

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: C82614

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: For a complete list of authors see reference number A59328 below

A:Accession: C82614

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-398 <SIM>

A:Cross-references: UNIPROT:Q9PBZ3; GB:AE004018; GB:AE003849; NID:g9107093; PIDN:AAF84794

A:Experimental source: strain 9a5c

R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki

A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1992

C:Superfamily: Azospirillum cyclohydrolase II; cyclohydrolase homology

Query Match 70.4%; Score 38; DB 2; Length 398;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAVLLPVLAAAP 12

DB 131 AALLPAIVAAAP 141

RESULT 10

D86957

A:Species: Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: D86957

R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; -Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D86957

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <STO>

Fri Feb 4 11:21:32 2005

A;Cross-references: GB:AL450380; NID:gl3092663; PIDN:CAC29896.1; GSPDB:GN00147

C;Genetics:

A;Gene: guaB3

C;Superfamily: Synchocystis IMP dehydrogenase homolog; IMP dehydrogenase amino-terminal

Query Match 68.5%; Score 37; DB 2; Length 370;
 Best Local Similarity 81.8%; Pred. No. 64;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11

| | | | |

Db 141 AAVLLPVLAA 151

RESULT 11

S72812 IMP dehydrogenase-related protein guaB1 - Mycobacterium leprae

N;Alternate names: B1620 C2_193 protein

C;Species: Mycobacterium leprae

C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 09-Jul-2004

C;Accession: S72812

R;Smith, D.R.; Robinson, K.

submitted to the EMBL Data Library, November 1993

A;Description: Mycobacterium leprae cosmid B1620.

A;Reference number: S72584

A;Accession: S72812

A;Molecule type: DNA

A;Residues: 1-375 <SMI>

A;Cross-references: UNIPROT:Q49721; EMBL:U00015; NID:g466931; PIDN:AAC43221.1; PID:g4669

C;Comment: This sequence is similar to IMP dehydrogenase at the amino end and at the car

name and GMP reductase.

C;Genetics:

A;Gene: guaB1

C;Superfamily: Synchocystis IMP dehydrogenase homolog; IMP dehydrogenase amino-terminal

F;14-79/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F;127-363/Domain: IMP dehydrogenase catalytic homology <IDHC>

Query Match 68.5%; Score 37; DB 1; Length 375;

Best Local Similarity 81.8%; Pred. No. 65;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11

| | | | |

Db 146 AAVLLPVLAA 156

RESULT 12

H82825

transport protein XF0281 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: H82825

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82825

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <SIM>

A;Cross-references: UNIPROT:Q9PGL7; GB:AE003881; GB:AE003849; NID:g9105093; PIDN:AAF8309

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0281

Query Match 68.5%; Score 37; DB 2; Length 389;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVLLPVLAA 10

| | | | |

Db 69 AAVLLPVLAA 77

RESULT 13

C75511 alanyl-tRNA synthetase-related protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: C75511

R;White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I

S.; Smith, H.O.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75511

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-409 <WHI>

A;Cross-references: UNIPROT:Q9RX13; GB:AE001909; GB:AE000513; NID:g6458188; PIDN:AAF1008

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0502

A;Map position: 1

Query Match 68.5%; Score 37; DB 2; Length 409;

Best Local Similarity 66.7%; Pred. No. 70;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12

| | | | |

Db 333 AAVLLPVLTAAP 344

RESULT 14

T05877

hypothetical protein T29A15.210 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05877

R;Bavan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Hol

submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15455

A;Accession: T05877

A;Molecule type: DNA

A;Residues: 1-420 <BEV>

A;Cross-references: UNIPROT:Q9T094; EMBL:AL035602

A;Experimental source: cultivar Columbia; BAC clone T29A15

C;Genetics:

A;Map position: 4

A;Introns: 51/1; 99/2; 155/3; 246/1; 334/3; 378/3

A;Note: T29A15.210

C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.170

Query Match 68.5%; Score 37; DB 2; Length 420;

Best Local Similarity 63.6%; Pred. No. 72;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11

| | | | |

Db 325 AALLFILMTA 335

RESULT 15

C95046
 helicasase, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: C95046
 R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: C95046
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-788 <KUR>
 A:Cross-references: UNIPROT:Q97SG8; GB:AE005672; PIDN:AAK74564.1; PID:gl4971869; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0401

Query Match 68.5%; Score 37; DB 2; Length 788;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVLLAAP 12
 ||:||||
 Db 384 LPVLLAAP 391

Search completed: February 2, 2005, 18:45:02
 Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:27:02 ; Search time 194 Seconds
(without alignments)
35.590 Million cell updates/sec

Title: US-10-634-645-1
Perfect score: 54
Sequence: 1 AAVLLPVLAAAP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 43 | 79.6 | 340 | 2 Q8FRS4 | Q8frs4 corynebacte |
| 2 | 43 | 77.8 | 291 | 2 Q98FS7 | Q98fs7 rhizobium 1 |
| 3 | 41 | 75.9 | 356 | 2 Q8H8C7 | Q8h8c7 oryza sativ |
| 4 | 40 | 74.1 | 133 | 2 Q6ND81 | Q6nd81 rhodospheuo |
| 5 | 40 | 74.1 | 133 | 2 CAE25672 | CAe25672 rhodospheu |
| 6 | 40 | 74.1 | 195 | 2 Q7PS92 | Q7ps92 anophelies g |
| 7 | 40 | 74.1 | 195 | 2 Q9BIH2 | Q9bih2 anophelies g |
| 8 | 40 | 74.1 | 279 | 2 Q89D56 | Q89d56 bradyrhizob |
| 9 | 40 | 74.1 | 390 | 2 Q9YDB2 | Q9ydb2 aeropyrum p |
| 10 | 40 | 74.1 | 497 | 2 Q6N2W2 | Q6n2w2 rhodospheuo |
| 11 | 40 | 74.1 | 497 | 2 CAE29377 | CAe29377 rhodospheu |
| 12 | 40 | 74.1 | 639 | 2 Q9K4H5 | Q9k4h5 streptomyce |
| 13 | 40 | 74.1 | 659 | 2 Q82NQ4 | Q82nq4 streptomyce |
| 14 | 40 | 74.1 | 831 | 2 Q89RR5 | Q89rr5 bradyrhizob |
| 15 | 40 | 74.1 | 1114 | 2 Q86XD7 | Q86xd7 homo sapien |
| 16 | 40 | 74.1 | 1247 | 1 NIDO_HUMAN | P14543 homo sapien |
| 17 | 39 | 72.2 | 43 | 1 PSBY_SYNEL | Q8dkm3 synecococc |
| 18 | 39 | 72.2 | 253 | 2 Q73HU0 | Q73hu0 wobbachia p |
| 19 | 39 | 72.2 | 253 | 2 AAS14173 | Aa14173 wobbachia |
| 20 | 39 | 72.2 | 303 | 2 Q91108 | Q91108 pseudomonas |
| 21 | 39 | 72.2 | 481 | 2 Q95W90 | Q95w90 trypsinosoma |
| 22 | 39 | 72.2 | 493 | 2 Q8U966 | Q8u966 agrobacteri |
| 23 | 39 | 72.2 | 498 | 2 Q7VU08 | Q7vu08 bordetella |
| 24 | 39 | 72.2 | 582 | 2 Q99PG1 | Q99pg1 cricetus |
| 25 | 39 | 72.2 | 602 | 2 Q7CTH2 | Q7cth2 agrobacteri |
| 26 | 39 | 72.2 | 628 | 2 Q89IJ7 | Q89ij7 bradyrhizob |
| 27 | 39 | 72.2 | 3970 | 2 Q93H18 | Q93h18 streptomyce |
| 28 | 38 | 70.4 | 38 | 1 PSBY_PROMM | P59909 prochloroco |
| 29 | 38 | 70.4 | 111 | 2 Q9NE12 | Q9ne12 leishmania |
| 30 | 38 | 70.4 | 131 | 2 Q8KP20 | Q8kp20 thermus the |
| 31 | 38 | 70.4 | 131 | 2 Q72JCO | Q72jco thermus the |

| | | | | | |
|----|----|------|-----|--------------|--------------------|
| 32 | 38 | 70.4 | 131 | 2 AAS81202 | Aa81202 thermus t |
| 33 | 38 | 70.4 | 175 | 1 DIAC_BOVIN | Q01458 bos taurus |
| 34 | 38 | 70.4 | 186 | 2 Q6Z3J4 | Q6z3j4 oryza sativ |
| 35 | 38 | 70.4 | 186 | 2 BAD16090 | Bad16090 oryza sat |
| 36 | 38 | 70.4 | 222 | 2 Q6CPR9 | Q6cpr9 kluyveromyc |
| 37 | 38 | 70.4 | 239 | 2 Q8XVC4 | Q8xvc4 ralstonia s |
| 38 | 38 | 70.4 | 240 | 2 Q7EYB9 | Q7eyb9 oryza sativ |
| 39 | 38 | 70.4 | 240 | 2 BAD01437 | Bad01437 oryza sat |
| 40 | 38 | 70.4 | 240 | 2 BAC99441 | Bac99441 oryza sat |
| 41 | 38 | 70.4 | 249 | 1 YEG0_STRCO | P40179 streptomyce |
| 42 | 38 | 70.4 | 278 | 1 Q89TK8 | Q89tk8 bradyrhizob |
| 43 | 38 | 70.4 | 293 | 2 Q8FYJ9 | Q8fyj9 brucella su |
| 44 | 38 | 70.4 | 297 | 2 Q8YJ99 | Q8yj99 brucella me |
| 45 | 38 | 70.4 | 397 | 2 Q752P8 | Q752p8 ashbya goss |

ALIGNMENTS

| | | | | | |
|---|---|--|--|--|--|
| RESULT 1 | | | | | |
| Q8FRS4 PRELIMINARY; PRT; 340 AA. | | | | | |
| ID | Q8FRS4 | | | | |
| AC | Q8FRS4; | | | | |
| DT | 01-MAR-2003 (Tremblrel. 23, Created) | | | | |
| DT | 01-MAR-2003 (Tremblrel. 23, Last sequence update) | | | | |
| DT | 01-OCT-2003 (Tremblrel. 25, Last annotation update) | | | | |
| DE | Putative iron transport membrane protein. | | | | |
| GN | OrderedLocustNames=CE0685; | | | | |
| OS | Corynebacterium efficiens. | | | | |
| OC | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; | | | | |
| OC | Corynebacterineae; Corynebacteriaceae; Corynebacterium. | | | | |
| OX | NCBI_TaxID=152794; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=YS-314; | | | | |
| RX | MEDLINE=22723752; PubMed=12840036; | | | | |
| RA | Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., | | | | |
| RA | Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., | | | | |
| RA | Gojobori T.; | | | | |
| RT | "Comparative complete genome sequence analysis of the amino acid | | | | |
| RT | replacements responsible for the thermostability of Corynebacterium | | | | |
| RT | efficiens." | | | | |
| RL | Genome Res. 13:1572-1579(2003). | | | | |
| DR | EMBL; AP005216; BAC17495.1; -- | | | | |
| DR | HSSP; P06609; 1LTV. | | | | |
| DR | GO; GO:0016020; C:membrane; IEA. | | | | |
| DR | GO; GO:0005215; F:transporter activity; IEA. | | | | |
| DR | GO; GO:0006810; P:transport; IEA. | | | | |
| DR | InterPro; IPR000522; FecD. | | | | |
| DR | Pfam; PF01032; FecCD; 1. | | | | |
| KW | Complete proteome. | | | | |
| SQ | SEQUENCE 340 AA; 34818 MW; 14B047C6A943A576 CRC64; | | | | |
| Query Match 79.6%; Score 43; DB 2; Length 340; | | | | | |
| Best Local Similarity 100.0%; Pred. No. 35; | | | | | |
| Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | |
| QY | 2 AVLLPVLAA 11 | | | | |
| | | | | | |
| Db | 211 AVLLPVLAA 220 | | | | |
| RESULT 2 | | | | | |
| Q98FS7 PRELIMINARY; PRT; 291 AA. | | | | | |
| ID | Q98FS7 | | | | |
| AC | Q98FS7; | | | | |
| DT | 01-OCT-2001 (Tremblrel. 18, Created) | | | | |
| DT | 01-OCT-2001 (Tremblrel. 18, Last sequence update) | | | | |
| DT | 01-MAR-2002 (Tremblrel. 20, Last annotation update) | | | | |
| DE | Mlr3636 protein. | | | | |
| GN | OrderedLocustNames=mlr3636; | | | | |
| OS | Rhizobium loti (Mesorhizobium loti). | | | | |
| OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; | | | | |

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;

[1]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214969;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RNA Res. 7:331-338(2000).

[2]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082936; PubMed=11214974;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

RNA Res. 7:381-406(2000).

EMBL; AP003002; BAB50490.1; -.

KW Complete proteome.

SQ SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 291;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAVLLPVLAAAP 12

DB 115 SAIFLPVIAAP 126

RESULT 3

Q8H8C7 PRELIMINARY; PRT; 356 AA.

AC Q8H8C7

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein O01006F06.19.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzoae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C., Currie J., Collura K.;

RL Submitted (SFP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC099399; AAN05509.1; -.

DR Granene; Q8H8C7; -.

DR GO; GO:0016998; P:cell wall catabolism; IEA.

DR InterPro; IPR002482; LysM.

DR Pfam; PF01476; LysM; 2.

DR SMART; SM00257; LysM; 2.

KW Hypothetical protein.

SQ SEQUENCE 356 AA; 37200 MW; 007D7BED10AB98FE CRC64;

Query Match 75.9%; Score 41; DB 2; Length 356;

Best Local Similarity 83.3%; Pred. No. 82;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAVLLPVLAAAP 12

DB 115 SAIFLPVIAAP 126

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;

[1]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214969;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RNA Res. 7:331-338(2000).

[2]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082936; PubMed=11214974;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

RNA Res. 7:381-406(2000).

EMBL; AP003002; BAB50490.1; -.

KW Complete proteome.

SQ SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 291;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAVLLPVLAAAP 12

DB 115 SAIFLPVIAAP 126

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;

[1]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214969;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RNA Res. 7:331-338(2000).

[2]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082936; PubMed=11214974;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

RNA Res. 7:381-406(2000).

EMBL; AP003002; BAB50490.1; -.

KW Complete proteome.

SQ SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 291;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAVLLPVLAAAP 12

DB 115 SAIFLPVIAAP 126

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;

[1]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214969;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RNA Res. 7:331-338(2000).

[2]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082936; PubMed=11214974;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

RNA Res. 7:381-406(2000).

EMBL; AP003002; BAB50490.1; -.

KW Complete proteome.

SQ SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 291;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAVLLPVLAAAP 12

DB 115 SAIFLPVIAAP 126

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;

[1]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214969;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

RNA Res. 7:331-338(2000).

[2]

SEQUENCE FROM N.A.

STRAIN=MAFF303099;

MEDLINE=21082936; PubMed=11214974;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";

RNA Res. 7:381-406(2000).

EMBL; AP003002; BAB50490.1; -.

KW Complete proteome.

SQ SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;

QY 1 AAVLLPVLAA 11
 DB 15 AAVLLPVLAA 25
 RESULT 6
 Q7PS92 PRELIMINARY; PRT; 195 AA.
 AC Q7PS92;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENSANGP0000018919.
 GN Name=ENSANGS0000016430;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008844; EAA05987.2; -.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PROSITE; P500141; ASP_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 195;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 12
 DB 14 AAVLLPVLAA 25
 RESULT 7
 Q9BIH2 PRELIMINARY; PRT; 195 AA.
 AC Q9BIH2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein gSG10 precursor.
 GN Name=gSG10;
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSUA;
 RX MEDLINE=22057806; PubMed=12062411;
 RA Lanfrancotti A., Lombardo F., Santolamazza F., Veneri M.,
 RA Castriagnano T., Coluzzi M., Arca' B.;
 RT "Novel cDNAs encoding salivary proteins from the malaria vector
 RT Anopheles gambiae.";
 RL FEBS Lett. 517:67-71 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSUA;
 RA Arca B.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ302660; CAC3525.1; -.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PROSITE; P500141; ASP_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 35 Potential.

SQ SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 195;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 12
 DB 14 AAVLLPVLAA 25
 RESULT 8
 Q89D56 PRELIMINARY; PRT; 279 AA.
 ID Q89D56;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE B1r7587 protein.
 GN OrderedLocusNames=b1r7587;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Iidesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197 (2002).
 DR EMBL; AP005962; BACS2852.1; -.
 KW Complete proteome.
 SQ SEQUENCE 279 AA; 29666 MW; 27651945C0E13C39 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 279;
 Best Local Similarity 58.3%; Pred. No. 98;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 12
 DB 115 AAVLLPVLAA 126
 RESULT 9
 Q9YDB2 PRELIMINARY; PRT; 390 AA.
 ID Q9YDB2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE1001.
 GN OrderedLocusNames=APE1001;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kwarababayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyana A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";

| | | | | | |
|-----------------------|---|-----------------------|---|-----------------------|---|
| RA | Harrison F.H., Gibson J., Harwood C.S.; | RA | "Complete genome sequence of the metabolically versatile | RA | Complete genome sequence of the metabolically versatile |
| RT | EMBL; AP000060; BAA79985.1; - | RT | phototrophic bacterium Rhodospirillum rubrum | RT | phototrophic bacterium Rhodospirillum rubrum |
| RL | PIR; A72698; A72698 | RL | Nat. Biotechnol. 22:55-61(2004). | RL | Nat. Biotechnol. 22:55-61(2004). |
| DR | Complete proteome; Hypothetical protein. | DR | EMBL; BX572605; CAE29377.1; - | DR | EMBL; BX572605; CAE29377.1; - |
| KW | Complete proteome; Hypothetical protein. | KW | Hypothetical protein; Signal. | KW | Hypothetical protein; Signal. |
| FT | SIGNAL 1 30 Potential. | FT | SIGNAL 1 30 Potential. | FT | SIGNAL 1 30 Potential. |
| SQ | SEQUENCE 390 AA; 41090 MW; 9898066EAEFDF207 CRC64; | SQ | SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64; | SQ | SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64; |
| Query Match | 74.1%; Score 40; DB 2; Length 390; | Query Match | 74.1%; Score 40; DB 2; Length 497; | Query Match | 74.1%; Score 40; DB 2; Length 497; |
| Best Local Similarity | 75.0%; Pred. No. 1.3e+02; | Best Local Similarity | 72.7%; Pred. No. 1.7e+02; | Best Local Similarity | 75.0%; Pred. No. 2.1e+02; |
| Matches | 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | Matches | 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0; | Matches | 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; |
| Qy | 1 AAVLLPVLAA 12 | Qy | 1 AAVLLPVLAA 11 | Qy | 1 AAVLLPVLAA 12 |
| Db | 180 AAKLPLLAAP 191 | Db | 20 AAVLPVLLAA 30 | Db | 7 AALLPLLGAP 18 |
| RESULT 10 | | RESULT 12 | | RESULT 13 | |
| ID | Q6N2W2 PRELIMINARY; PRT; 497 AA. | ID | Q9K4H5 PRELIMINARY; PRT; 639 AA. | ID | Q82N04 PRELIMINARY; PRT; 659 AA. |
| AC | Q6N2W2; 27, Created) | AC | Q9K4H5; 15, Last sequence update) | AC | Q82N04; 24, Last sequence update) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) | DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) | DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) |
| DE | Hypothetical protein precursor. | DE | Hypothetical protein precursor. | DE | Putative secreted amidase. |
| GN | OrderedLocusNames=RPA3936; | GN | OrderedLocusNames=SCO7250; | GN | OrderedLocusNames=SCO7250; |
| OS | Rhodospirillum rubrum | OS | Streptomyces coelicolor | OS | Streptomyces coelicolor |
| OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; | OC | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; | OC | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; |
| OC | Bradyrhizobiaceae; Rhodospirillum rubrum | OC | Streptomycetaceae; Streptomycetaceae; Streptomycetes. | OC | Streptomycetaceae; Streptomycetaceae; Streptomycetes. |
| OX | NCBI_TaxID=1076; | OX | NCBI_TaxID=1902; | OX | NCBI_TaxID=1902; |
| RN | [1] | RN | [1] | RN | [1] |
| RP | SEQUENCE FROM N.A. | RP | SEQUENCE FROM N.A. | RP | SEQUENCE FROM N.A. |
| RC | STRAIN=CGA009 / ATCC BAA-98; | RC | STRAIN=A3(2) / M145; | RC | STRAIN=A3(2) / M145; |
| RC | PubMed=14704707; DOI=10.1038/nbt923; | RC | MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a; | RC | MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a; |
| RA | Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., | RA | Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., | RA | Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., |
| RA | Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., | RA | Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., | RA | Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., |
| RA | Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C., | RA | Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., | RA | Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., |
| RA | Harrison F.H., Gibson J., Harwood C.S.; | RA | Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., | RA | Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., |
| RT | "Complete genome sequence of the metabolically versatile | RT | Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S., | RT | Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S., |
| RT | phototrophic bacterium Rhodospirillum rubrum | RT | Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S., | RT | Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S., |
| RT | Nat. Biotechnol. 22:55-61(2004). | RT | Seeger K., Saunders D., Sharp S., Squares S., Taylor K., | RT | Seeger K., Saunders D., Sharp S., Squares S., Taylor K., |
| DR | EMBL; BX572605; CAE29377.1; - | DR | Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., | DR | EMBL; BX572605; CAE29377.1; - |
| KW | Complete proteome; Hypothetical protein; Signal. | KW | Hopwood D.A.; | KW | Complete proteome; Hypothetical protein; Signal. |
| FT | SIGNAL 1 30 Potential. | FT | SIGNAL 1 30 Potential. | FT | SIGNAL 1 30 Potential. |
| SQ | SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64; | SQ | SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64; | SQ | SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64; |
| Query Match | 74.1%; Score 40; DB 2; Length 497; | Query Match | 74.1%; Score 40; DB 2; Length 497; | Query Match | 74.1%; Score 40; DB 2; Length 639; |
| Best Local Similarity | 72.7%; Pred. No. 1.7e+02; | Best Local Similarity | 72.7%; Pred. No. 1.7e+02; | Best Local Similarity | 75.0%; Pred. No. 2.1e+02; |
| Matches | 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0; | Matches | 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0; | Matches | 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; |
| Qy | 1 AAVLLPVLAA 11 | Qy | 1 AAVLLPVLAA 11 | Qy | 1 AAVLLPVLAA 12 |
| Db | 20 AAVLPVLLAA 30 | Db | 20 AAVLPVLLAA 30 | Db | 7 AALLPLLGAP 18 |
| RESULT 11 | | RESULT 11 | | RESULT 13 | |
| ID | CAE29377 PRELIMINARY; PRT; 497 AA. | ID | CAE29377 PRELIMINARY; PRT; 497 AA. | ID | Q82N04 PRELIMINARY; PRT; 659 AA. |
| AC | CAE29377; 27, Created) | AC | CAE29377; 27, Created) | AC | Q82N04; 24, Last sequence update) |
| DT | 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) | DT | 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) | DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) |
| DT | 02-MAR | | | | |

OrderedLocusNames=SAVL238;
 GN Streptomyces avermitilis;
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NA-4680;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005026; BAC68948.1;
 DR GO; GO:0008745; P:N-acetylmuramoyl-L-alanine amidase activity; IEA.
 DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
 DR InterPro; IPR002502; Amidase_2.
 DR Pfam; PF01510; Amidase_2; 1.
 DR SMART; SM00644; Ami_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 659 AA; 70218 MW; BA3905045D2792FF CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 659;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAVLLPVLIAAP 12
 DB 27 AALLPLLIAGAP 38
 ||:|||||
 RESULT 14
 Q89RR5 PRELIMINARY; PRT; 831 AA.
 AC Q89RR5
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE VirA-like protein.
 GN Name=VirA; OrderedLocusNames=blr2697;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsuoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 CC -1- SIMILARITY: Contains 1 histidine kinase domain.
 DR EMBL; AP005944; BAC47962.1;
 DR HSSP; P23837; 11D0.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO; GO:0000760; P:sensory perception; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pr_C.
 DR InterPro; IPR011006; Chey_like.
 DR InterPro; IPR005467; His_Kinase.
 DR InterPro; IPR003661; His_kin_N.
 DR InterPro; IPR009082; His_kin_homodim.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00512; HsKA; 1.
 DR Pfam; PF00072; Response_reg; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HsKA; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS0109; HIS_KIN; 1.
 DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW Transferase.
 SQ SEQUENCE 831 AA; 89854 MW; F15F92E7446541E0 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 831;
 Best Local Similarity 66.7%; Pred. No. 2.7e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLIAAP 12
 DB 768 AAPALPILIAAP 779
 ||:|||||
 RESULT 15
 Q86XD7 PRELIMINARY; PRT; 1114 AA.
 AC Q86XD7
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE NID protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE-Testis;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC045606; AAH45606.1; -.
DR HSSP; P10493; 1GL4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR011044; A:amine DH B like.
DR InterPro; IPR000152; ASX_HYDROXYL_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006605; G2F.
DR InterPro; IPR009017; GFP like.
DR InterPro; IPR06210; IEGF.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR010362; NIDO.
DR InterPro; IPR003886; Nidogen ext.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07474; G2F; 1.
DR Pfam; PF00058; Ldl_recept_b; 3.
DR Pfam; PF06119; NIDO; 1.
DR Pfam; PF00086; Thyroglobulin_1; 1.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00682; G2F; 1.
DR SMART; SM0135; LY; 5.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW EGF-like domain.
SQ SEQUENCE 1114 AA; 122099 MW; 854FC97ADFCC75D2 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 1114;
Best Local Similarity 72.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AVILPVLLAP 12
Db 15 ALLPLLLAGP 25

Search completed: February 2, 2005, 18:44:09
Job time: 198 secs